REMARKS

The present Amendment is in response to the Examiner's Office Action mailed November 26, 2003. Claims 5-7 are canceled. Claims 1-4, 10-15 and 18-19 are amended. Claims 1-4 and 8-19 are now pending.

Applicants expression their appreciation to the Examiner for conducting a telephone interview with Applicants on April 7, 2004. Reconsideration of the application is respectfully requested in view of the above amendments to the claims and the following remarks. For the Examiner's convenience and reference, Applicants' remarks are presented in the order in which the corresponding issues were raised in the Office Action.

I. Rejections under 35 U.S.C. § 112, First Paragraph

Claims 1-19 stand rejected under 35 U.S.C. § 112, First Paragraph for failing to comply with the written description requirement. Specifically, the Examiner reiterates that the claimed method for screening for transcription factor modulators is not adequately described in the disclosure; and the disclosure does not describe a single or any transcription factors (tf) modulators that has been identified or screened by the method.

As explained by Applicants during the telephone interview, independent claim 1 as amended specifies a method for screening a plurality of different agents as transcription factor modulators. **Each** of the agents is tested **one-by-one** for modulating transcription factors in a test sample of cells. The activated transcription factors present in the test sample are compared with those present in a control cell sample which is not contacted with the agent. The difference in the presence of transcription factors between the test and control sample indicates transcription modulation by the agent which was contacted with the test sample.

As discussed in detail in Applicants' Amendment filed on September 8, 2003, an example of such a transcription modulator is PMA (phorbol ester). PMA was found to be able to modulate transcription factor activities in cancer cells such as HeLa, A431, Jurkat, K-562, and Y79 cells. For example, a number of transcription factors including Ets and NF-E1 can be seen to have been activated at higher levels in the PMA-treated HeLa cells as compared to the HeLa cells not treated with PMA. Other agents can be tested for transcription modulation by following a procedure similar to that for testing PMA on various cell samples.

In view of the detailed description and ample examples provided in the specification, Applicants submit that the claimed invention is adequately described to convey to one skilled in the relevant art that the inventors at the time the application was filed, had possession of the claimed invention under 35 U.S.C. §112, First Paragraph. Withdrawal of this ground of rejection is respectfully requested.

II. Rejections under 35 U.S.C. § 112, Second Paragraph

The Examiner rejects claims 1-19 under 35 U.S.C. § 112, Second Paragraph for being indefinite for failing to particularly point out and distinctly claims the subject matter which applicant regards as the invention.

Applicants cancel claims 5-7 and amend claims 1-4, 10-15 and 18-19 to clarify the invention recited therein. Withdrawal of the rejection under 35 U.S.C. § 112, Second Paragraph is therefore respectfully requested.

III. Rejection under 35 U.S.C. § 103(a)

The Examiner rejects claims 1-19 rejected under 35 U.S.C. §103(a) as being unpatentable over Weissman et al. (U.S. Patent No. 6,066,452).

Independent claim 1 as amended specifies a method for screening a plurality of different agents as transcription factor modulators by comparing multiple different transcription factors in cell samples treated with or without any of the different agents. Specifically, the presence of the multiple different transcription factors in the cell samples is detected by using a library of nucleic acid probes **each of which comprises a recognition sequence** that **varies within the library** of the nucleic acid probes. **Each** of the **different** recognition sequences is **known** to bind to an activated **known transcription factor**. Such a library of the probes is then contacted with the test sample to form nucleic acid probe-transcription factor complexes. After isolation of the complexes, the nucleic acid probes that hybridize to the hybridization probes in an array are identified. Because the nucleic acid probes comprise recognition sequences that are already known to bind the activated known transcription factors, the known transcription factors activated in the test sample are identified based on the identities of the probes.

In contrast, Weissman et al discloses a method for identifying new pairs of transcription factor-DNA binding sites by using a library of nucleic acid probes with **randomized** sequences. Column 2, lines 4-15. Specifically, Weissman et al. teaches using a library of oligonucleotide

probes having randomized sequences –NNNNNNNNN- (column 12, line 49) to "fish out" transcription factors that can bind to any of the randomized DNA sequences (column 13, Table 3). Thus, Weissman et al. **did not start the screening** with a library of oligonucleotide probes with known sequences, and these random sequences are **not known to bind to any known transcription factors** in the sample **before the screening**. If Weissman et al. used the library of nucleic acid probes as claimed by Applicants, **their purpose of finding new transcription factors would be defeated** because the probes are already known to bind to known transcription factors.

In view of the distinct differences between claimed method and that disclosed in Weissman et al., the claimed invention is non-obvious under 35 U.S.C. §103(a). Withdrawal of the rejection is therefore respectfully requested.

CONCLUSION

In light of the remarks and arguments set forth above, Applicants earnestly believe that they are entitled to a letters patent, and respectfully solicit the Examiner to expedite prosecution of this patent application to issuance. Should the Examiner have any questions, the Examiner is encouraged to telephone the undersigned.

Respectfully submitted,

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